

Amendments to the Specification

These amendments insert sequence identifiers into the specification where appropriate. The undersigned hereby verifies that these amendments do not introduce new matter into the specification.

The page and line numbers correspond to the originally filed specification.

At the indicated page and line number, please replace the existing paragraphs with the following paragraphs:

(Page 12, line 27)

Where desired, one or more pairs of "adaptor" oligonucleotides may be used to bridge the cloning ends of the DNA fragments of interest (i.e. from the layer(s) in the desired sub-set) and the cloning site of the vector(s). The adaptor sequences have appropriate restriction site sequences (fragment and vector) at each end and a core sequence in the middle. An example core sequence is 5-CGTAGACGATGCGTGAGAC-3. (SEQ ID NO: 1)

(Page 23, line 1)

For ligation, enhancing linkers can be designed to avoid chimerical sequences and restoring the undesired restriction site during ligation. In the Examples herein, each linker consists of two oligos. The core sequences were 5'-TTGGCGTTTAC-3' (SEQ ID NO:2) and 3'-CCGCAAATG-5'.

(Page 24, line 26)

The digested DNA was purified using QIAQuick PCR purification kit, QiaGen. The purified DNA was eluted in 20 µl water and subsequently 5µl of the purified DNA fragments were used in a 10µl ligation reaction. Six oligos (as three enhancing linkers for HpaII, AluI and DraI) were added into the reaction. They were 5'-TTGGCGTTTAC-3' (SEQ ID NO: 2), 5'-CGGTAAACGCC-3' (SEQ ID NO: 3), 5'-TTGGCGTTTAC-3' (SEQ ID NO: 2), 5'-GTAAACGCC-3', 5'-TTGGCGTTTAC-3' (SEQ ID NO: 2), 5'-AATTGTAAACGCC-3' (SEQ ID

NO: 4) (see Table 1). The final concentration of each oligo was 0.1 μ M. One μ l of ligase was used and 0.2 μ g pZero vector (InvitroGen) digested with PstI was added. The reaction was at 15°C for 30 minutes and then kept at -20°C for subsequent transformation.

(Page 27, line 9, "Table 1")

Acc I

5'-TTGGCGTTTAC-3' (SEQ ID NO: 2)

5'-ATGTAAACGCC-3' (SEQ ID NO: 5)

5'-CGGTAAACGCC-3' (SEQ ID NO: 3)

Aci I

5'-TTGGCGTTTAC-3' (SEQ ID NO: 2)

5'-CGGTAAACGCC-3' (SEQ ID NO: 3)

Afl III

5'-TTGGCGTTTAC-3' (SEQ ID NO: 2)

5'-CUYGGTAAACGCC-3' (SEQ ID NO: 6)

Alu I

5'-TTGGCGTTTAC-3' (SEQ ID NO: 2)

5'-GTAAACGCC-3'

Apo I

5'-TTGGCGTTTAC-3' (SEQ ID NO: 2)

5'-AATTGTAAACGCC-3' (SEQ ID NO: 4)

Ban I

5'-TTGGCGTTTAC-3' (SEQ ID NO: 2)

5'-GYUCGTAAACGCC-3' (SEQ ID NO: 7)

Ban II

5'-TTGGCGTTTACUGCY-3' (SEQ ID NO: 8)

5'-GTAAACGCC-3'

Bfa I

5'-TTGGCGTTTAC-3' (SEQ ID NO: 2)

5'-TAGTAAACGCC-3' (SEQ ID NO: 9)

BsaA I

5'-TTGGCGTTTAC-3' (SEQ ID NO: 2)

5'-GTAAACGCC-3'

BsaH I

5'-TTGGCGTTTAC-3' (SEQ ID NO: 2)

5'-CGGTAAACGCC-3' (SEQ ID NO: 3)

BsaJ I

5'-TTGGCGTTTAC-3' (SEQ ID NO: 2)

5'-CNNGGTAAACGCC-3' (SEQ ID NO: 10)

BsiE I

5'-TTGGCGTTTACUY-3' (SEQ ID NO: 11)

5'-GTAAACGCC-3'

BssK I

5'-TTGGCGTTTAC-3' (SEQ ID NO: 2)

5'-CCNGGGTAAACGCC-3' (SEQ ID NO: 12)

BstN I

None is needed.

BstU I

5'-TTGGCGTTTAC-3' (SEQ ID NO: 2)

5'-GTAAACGCC-3'

Btg I

5'-TTGGCGTTTAC-3' (SEQ ID NO: 2)

5'-CUYGGTAAACGCC-3' (SEQ ID NO: 6)

Cac8 I

5'-TTGGCGTTTAC-3' (SEQ ID NO: 2)

5'-GTAAACGCC-3'

DpnI

5'-TTGGCGTTTAC-3' (SEQ ID NO: 2)

5'-GTAAACGCC-3'

Dpn II

5'-TTGGCGTTTAC-3' (SEQ ID NO: 2)

5'-GATCGTAAACGCC-3' (SEQ ID NO: 13)

Dra I

5'-TTGGCGTTTAC-3' (SEQ ID NO: 2)

5'-AATTGTAAACGCC-3' (SEQ ID NO: 4)

Eae I

5'-TTGGCGTTTAC-3' (SEQ ID NO: 2)
5'-GGCCGTAAACGCC-3' (SEQ ID NO: 14)
Fnu4H I
None is needed.
Hae II
5'-TTGGCGTTTACGCGC-3' (SEQ ID NO: 15)
5'-GTAAACGCC-3'
Hae III
5'-TTGGCGTTTAC-3' (SEQ ID NO: 2)
5'-GTAAACGCC-3'
Hha I
5'-TTGGCGTTTACCG-3' (SEQ ID NO: 16)
5'-GTAAACGCC-3'
Hinc II
5'-TTGGCGTTTAC-3' (SEQ ID NO: 2)
5'-GTAAACGCC-3'
Hinf I
5'-TTGGCGTTTAC-3' (SEQ ID NO: 2)
5'-ANTGTAAACGCC-3' (SEQ ID NO: 17)
HinP1 I
5'-TTGGCGTTTAC-3' (SEQ ID NO: 2)
5'-CGGTAAACGCC-3' (SEQ ID NO: 3)
Hpa II
5'-TTGGCGTTTAC-3' (SEQ ID NO: 2)
5'-CGGTAAACGCC-3' (SEQ ID NO: 3)
Hpy188 I
None is needed.
HpyCH4 III
None is needed.
HpyCH4 IV
5'-TTGGCGTTTAC-3' (SEQ ID NO: 2)
5'-CGGTAAACGCC-3' (SEQ ID NO: 3)
HpyCH4 V
5'-TTGGCGTTTAC-3' (SEQ ID NO: 2)

5'-GTAAACGCC-3'

Mbo I

5'-TTGGCGTTTAC-3' (SEQ ID NO: 2)

5'-GATCGTAAACGCC-3' (SEQ ID NO: 13)

Mnl I

None is needed.

Mse I

5'-TTGGCGTTTAC-3' (SEQ ID NO: 2)

5'-TAGTAAACGCC-3' (SEQ ID NO: 9)

Msl I

None is needed.

Msp I

5'-TTGGCGTTTAC-3' (SEQ ID NO: 2)

5'-CGGTAAACGCC-3' (SEQ ID NO: 3)

Nla III

5'-TTGGCGTTTACCATG-3' (SEQ ID NO: 18)

5'-GTAAACGCC-3'

Nla IV

5'-TTGGCGTTTAC-3' (SEQ ID NO: 2)

5'-GTAAACGCC-3'

Nsp I

5'-TTGGCGTTTACCATG-3' (SEQ ID NO: 18)

5'-GTAAACGCC-3'

Rsa I

5'-TTGGCGTTTAC-3' (SEQ ID NO: 2)

5'-GTAAACGCC-3'

*Sau*3A I

5'-TTGGCGTTTAC-3' (SEQ ID NO: 2)

5'-GATCGTAAACGCC-3' (SEQ ID NO: 13)

*Sau*96 I

5'-TTGGCGTTTAC-3' (SEQ ID NO: 2)

5'-GNCGTAAACGCC-3' (SEQ ID NO: 19)

*Scr*F I

None is needed.

Sfc I

5'-TTGGCGTTTAC-3' (SEQ ID NO: 2)

5'-TUYAGTAAACGCC-3' (SEQ ID NO: 20)

Sml I

5'-TTGGCGTTTAC-3' (SEQ ID NO: 2)

5'-TYUAGTAAACGCC-3' (SEQ ID NO: 21)

Taq I

5'-TTGGCGTTTAC-3' (SEQ ID NO: 2)

5'-CGGTAAACGCC-3' (SEQ ID NO: 3)

Tsp509 I

5'-TTGGCGTTTAC-3' (SEQ ID NO: 2)

5'-AATTGTAAACGCC-3' (SEQ ID NO: 4)

CviJ I

None is needed.

CviT I

None is needed.